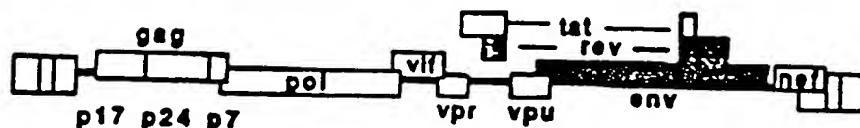




A



B

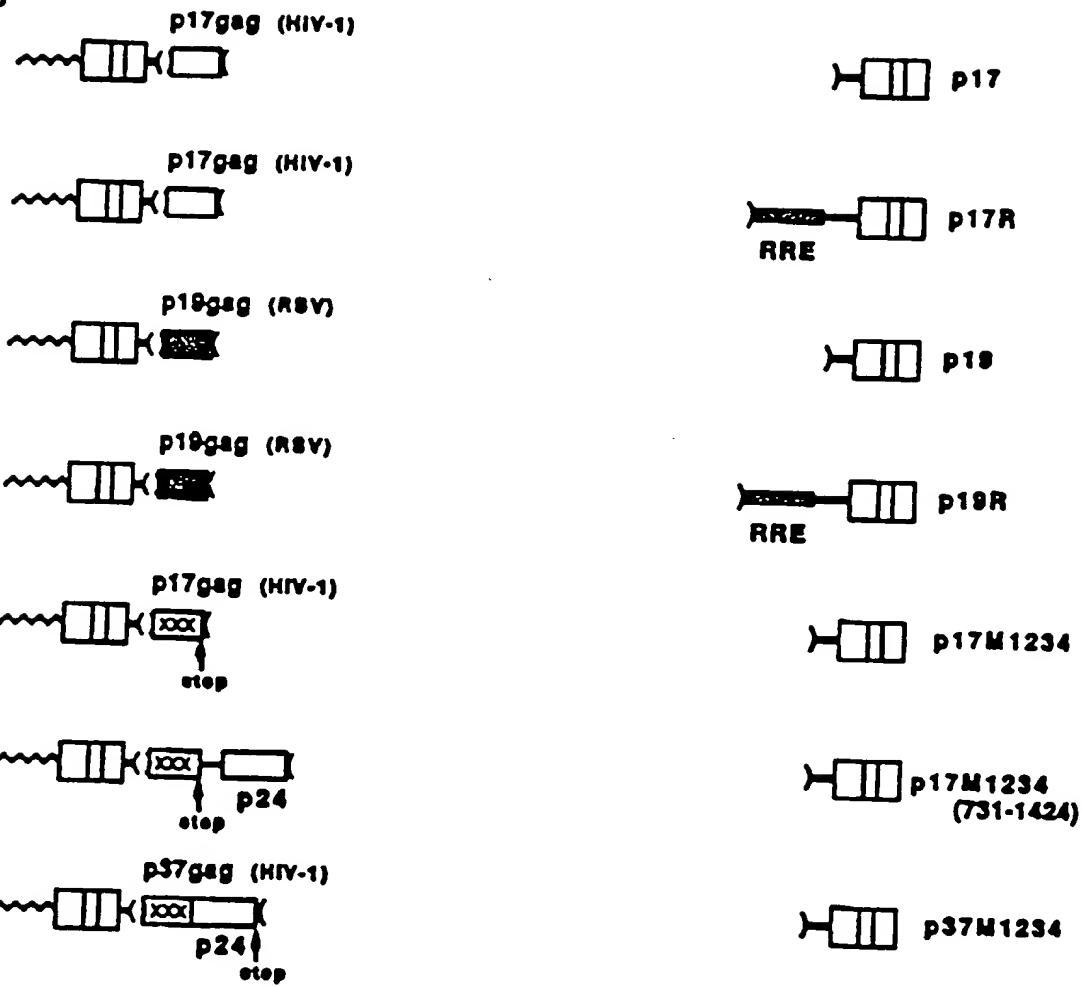


Figure 1



C

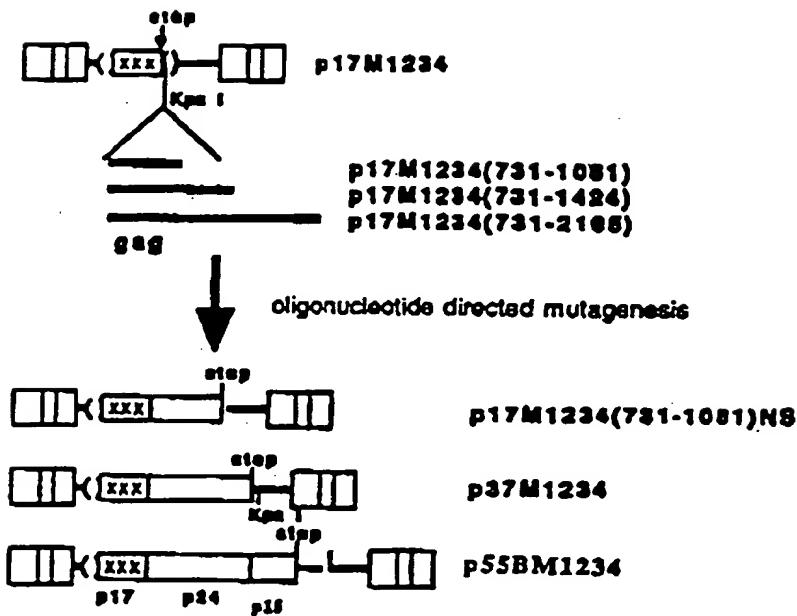
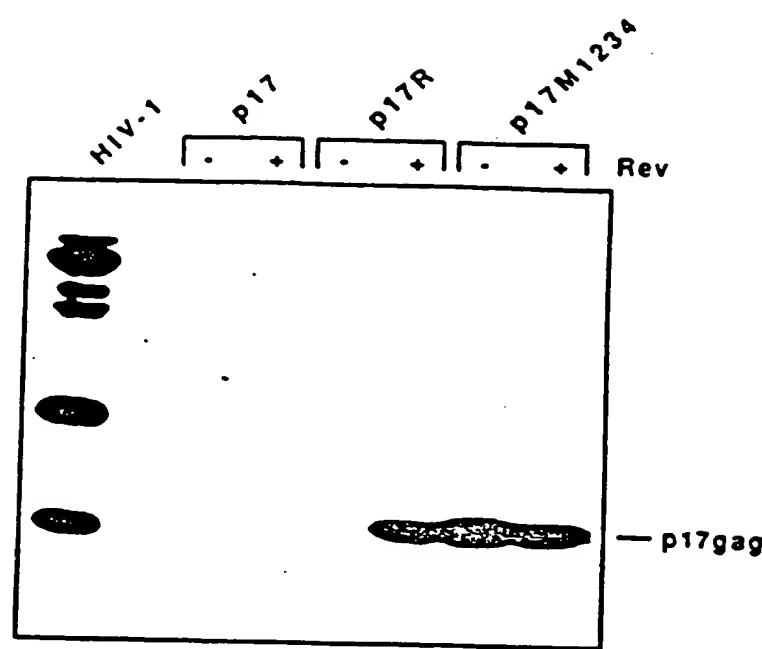


Figure 1 continued



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A



B

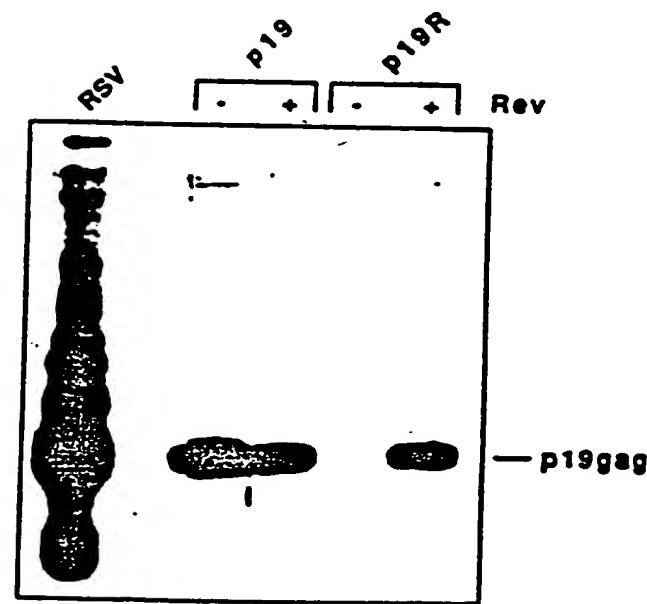
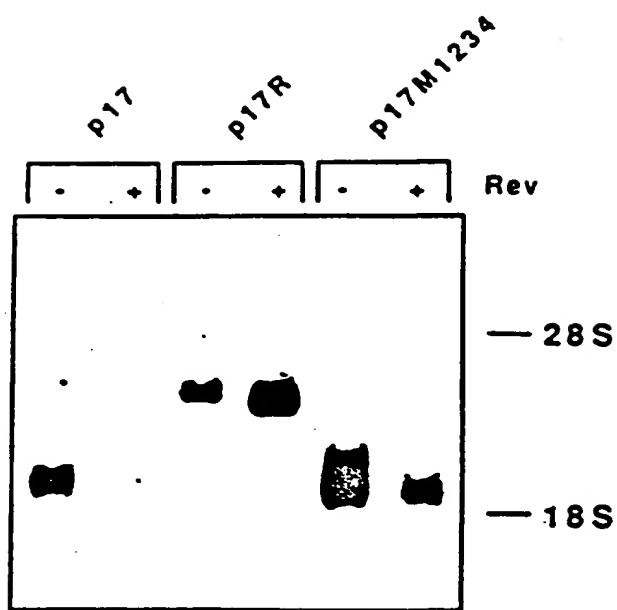


Figure 2



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A



B

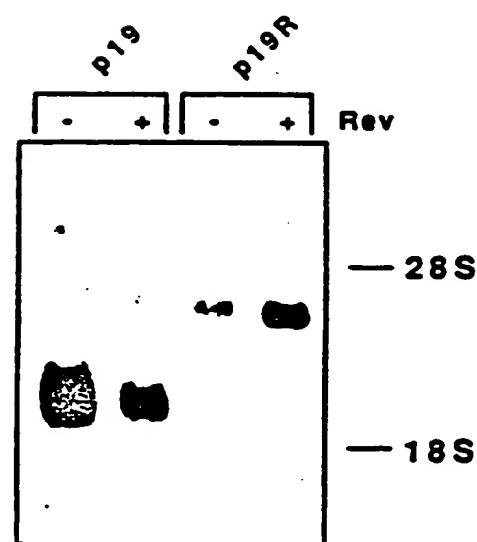


Figure 3



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336 acg ggt gcg aga gcg tca gta tta agc ggg gga gaa tta gat cga tgg gaa aca att cgg
 396 tta agg cca ccc gga aag aca aaa tat aaa tta aaa cat ata gca tgg gca agc agg gag
 436 G G C G C G C C
 cta gaa cga ttc gca gtt aat cct ggc ctg tta gaa aca tca gaa ggc tgt aga caa ata
 516 ctg gga cag cta caa cca tcc ccc caq aca gga tca gaa aaa ccc aqa tca tta tat aat
 576 G G C C C C
 636 aca ata gca acc ttc tat tct tgg cat caa agg ata gag ata aaa gac acc agg gaa gct
 696 G G C C G
 696 tta gac aag ata gag gaa gag caa acc aaa agt agg aaa aaa gca caq caa gca gca gct
 696 G TCC G G C G

Figure 4

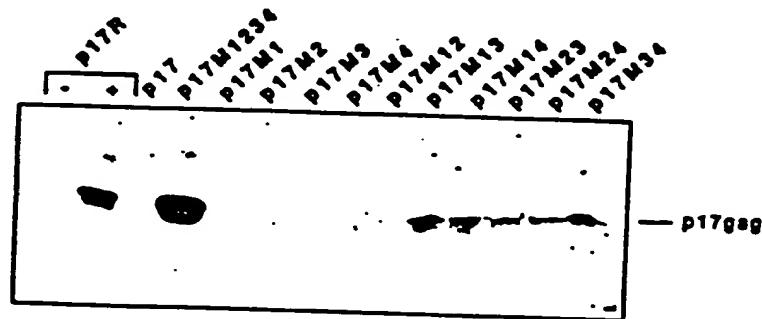


Figure 5



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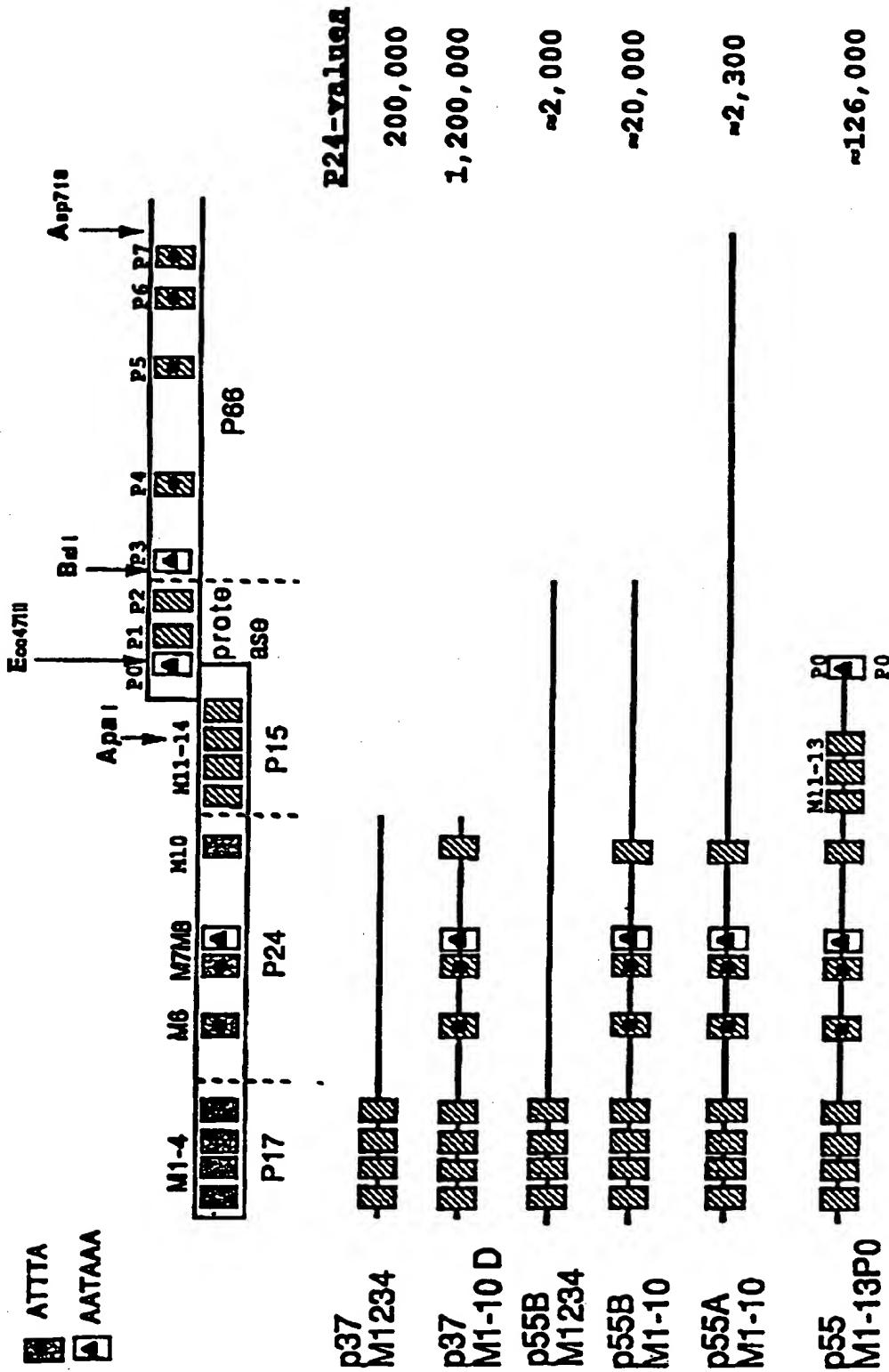


Figure 6



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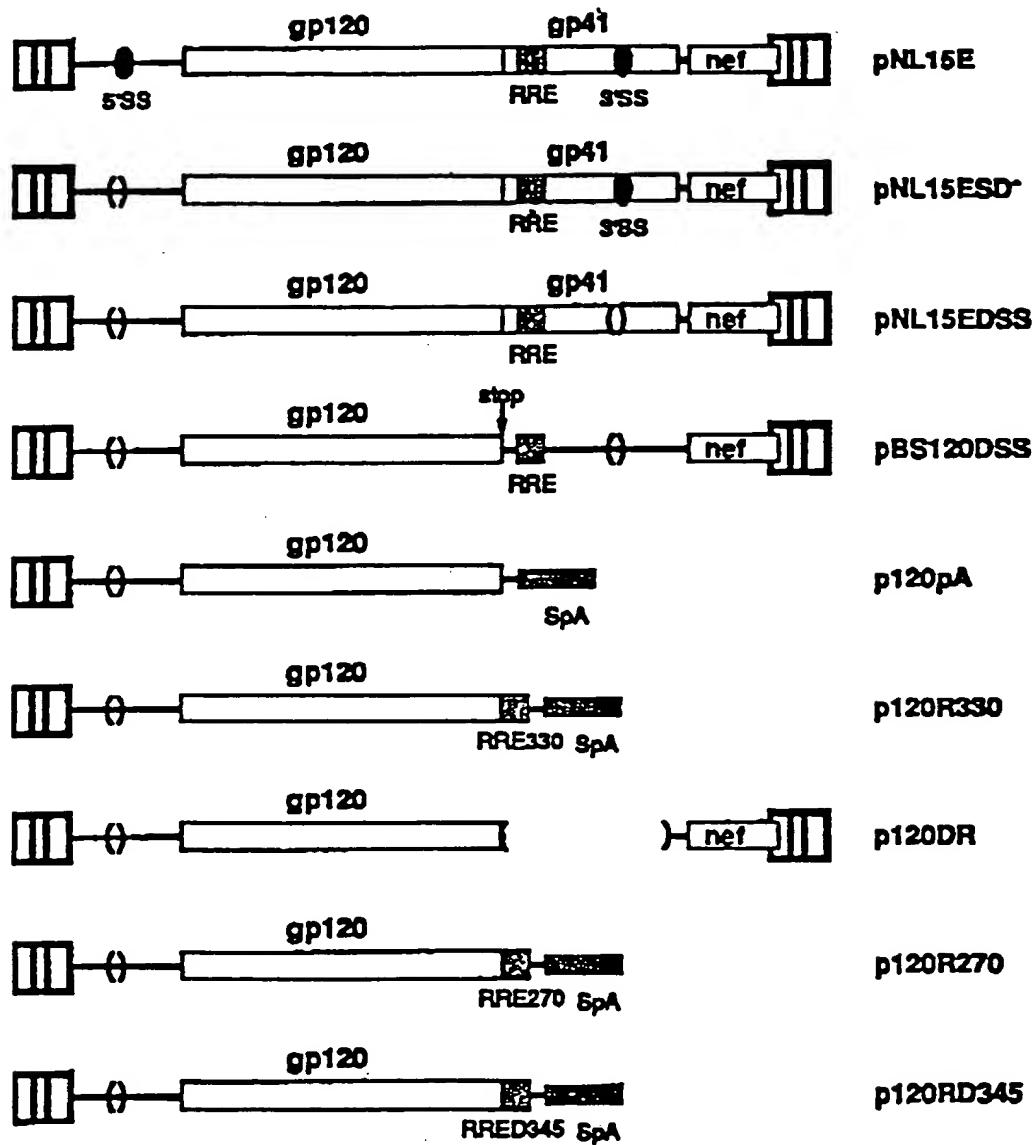
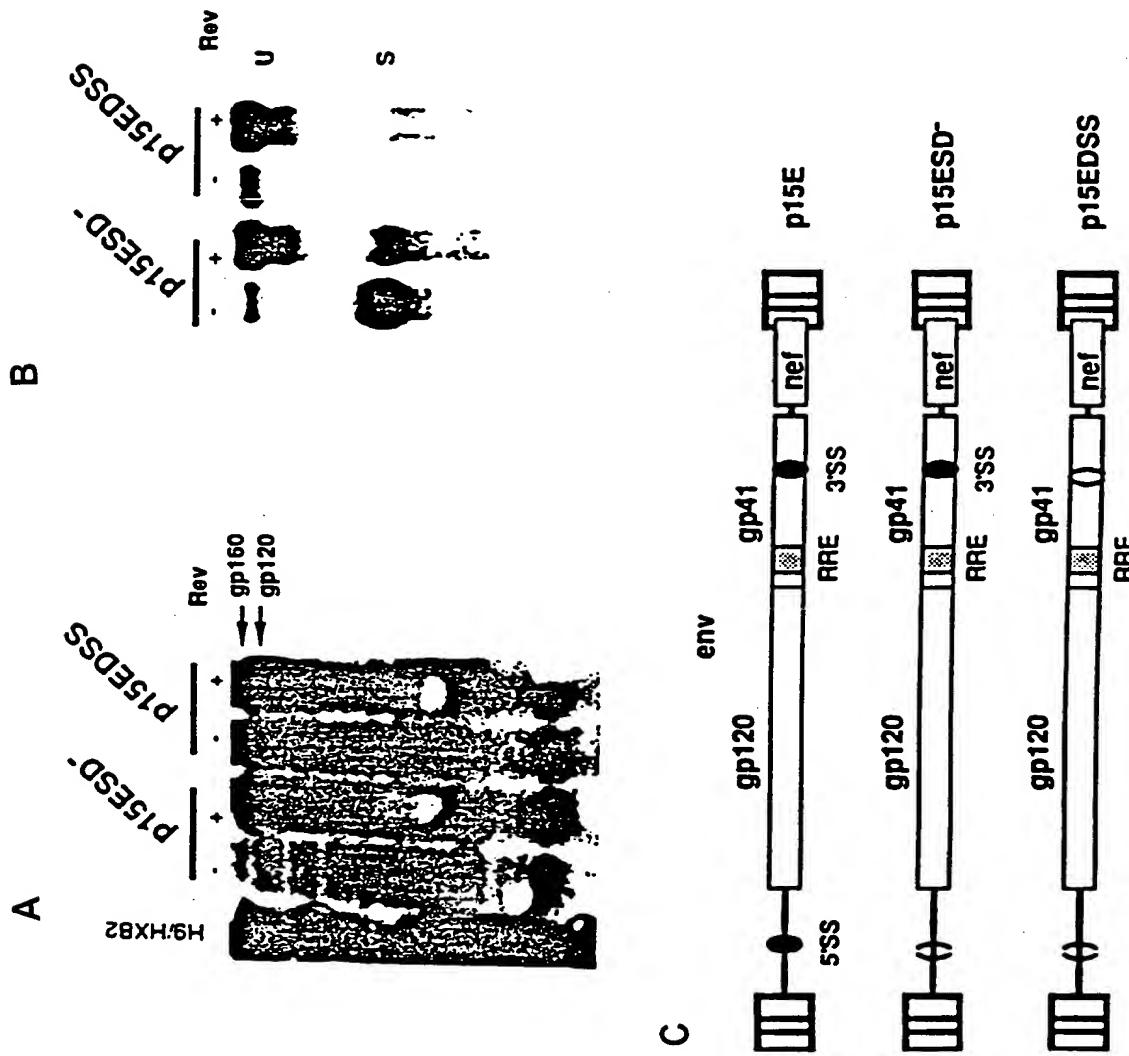


Figure 7



Figure 8





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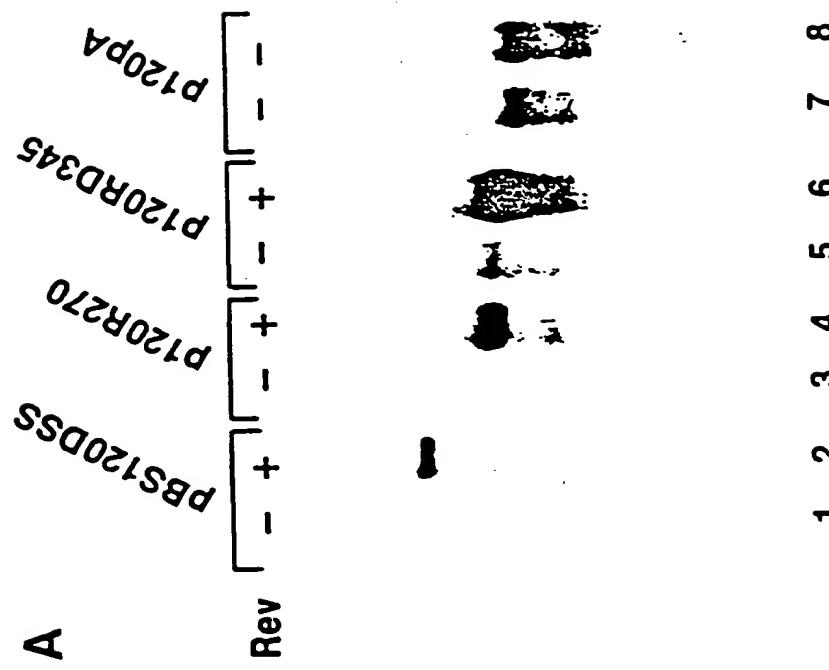


Figure 9



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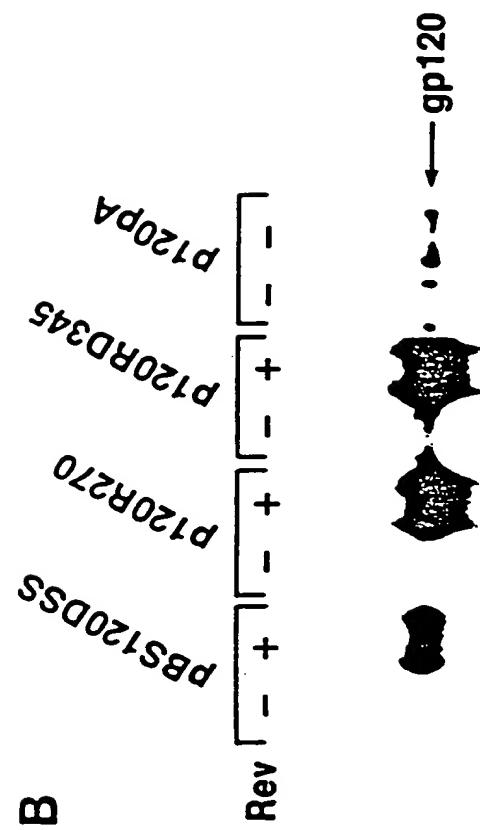
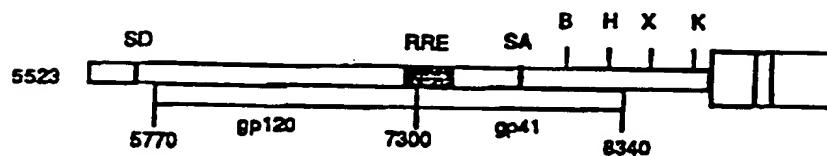


Figure 9



**Identification of INS regions within the
env mRNA using the p19 vector.**



<u>FRAGMENT SIZE</u>		<u>INS EFFECT</u>
A 276	██████ 7884-7859	none
B 234	██████ 7884-7884, 7927-7859	none
C 323	██████ 7595-7884, 7927-7859	10 X
D 128	████ 7839-8066	none
E 478	██████████ 7939-8416	10 X
F 362	██████████ 8290-8581	> 100 X
G 330	████ 7266-7595	3-5X
E 668 ██████████ 5523-6190		10 X

Figure 10



Identification of INS regions within the env mRNA using the p37M1-10D vector.

Digitized by srujanika@gmail.com

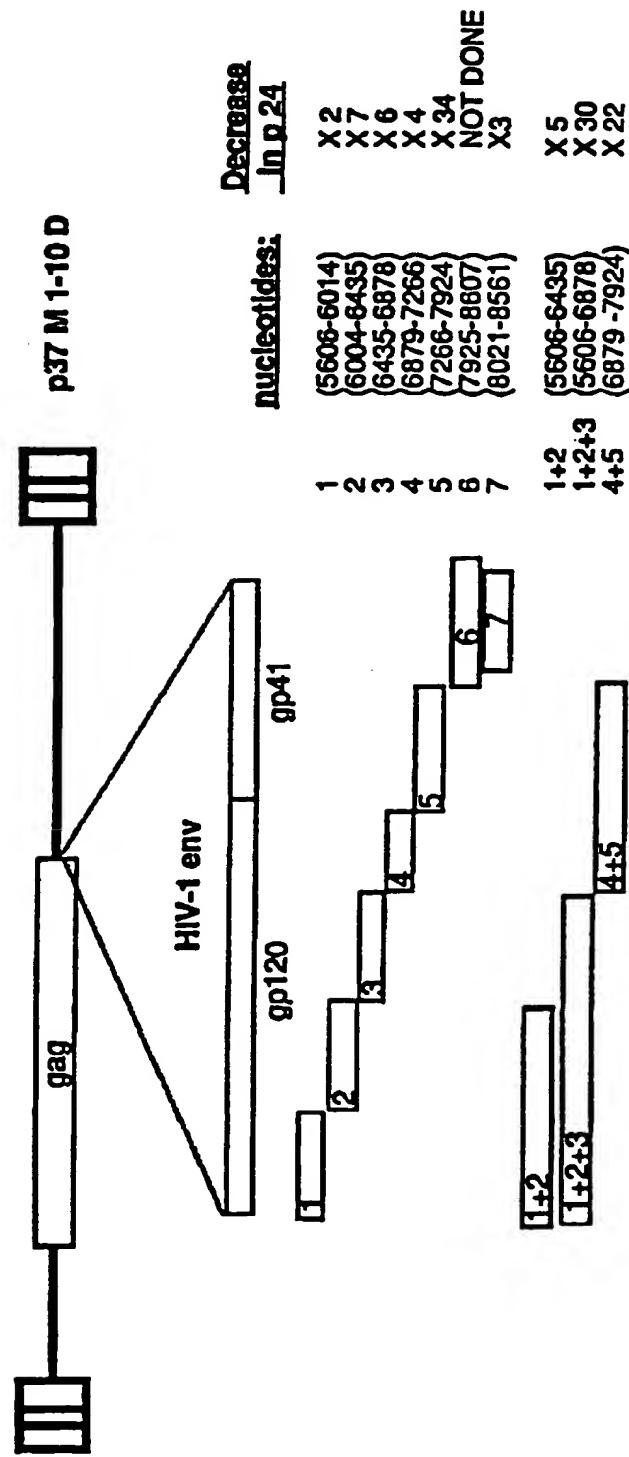


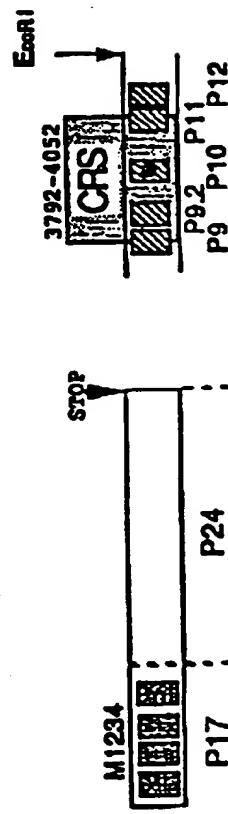
Figure 11



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Elimination of negative effects of CRS

ATTN:



level of P24 expression

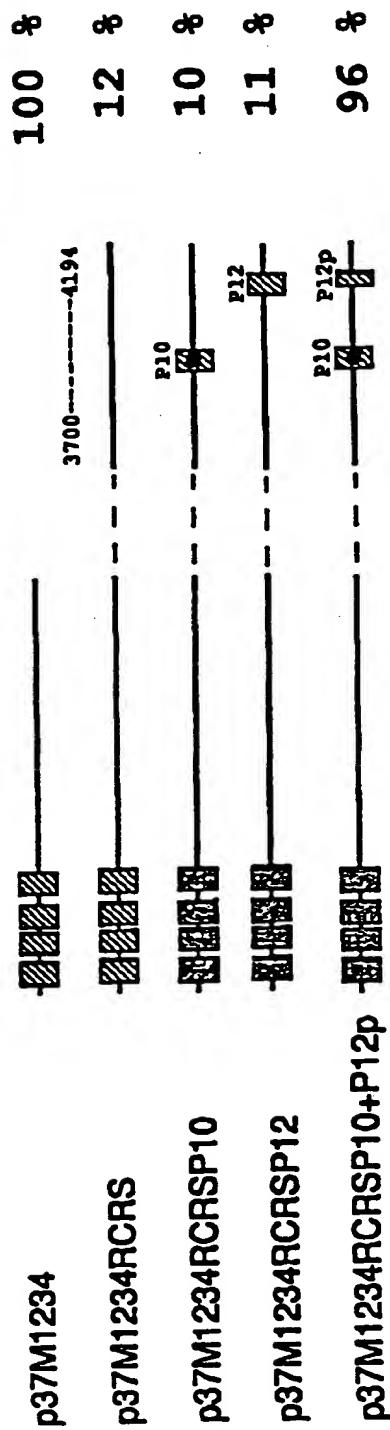


Figure 12



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POINT MUTATIONS ELIMINATING THE NEGATIVE EFFECTS OF CRS IN THE pol REGION
(nucleotides 3700-4194) (SEQ ID NO:127)

GGTACCCAGCACACAAAGGAAATTGGGAAATGAAACAAGTAGATAAATTAGTCAGTCCTCGAAATTCAGGAAGTACTTTT
TAGATGGATAAGATAAGGCCCAAGATGAACATGAAUATATCACAGTAATTGGAGAGCAATTCAGCTAGCTGATTTAACCTG
CCACCTGTAGTAGGAAAAGAAATATAGGCCAGCTGTGATAAATGTCAGCTAAAGGAGAGCCATGCAATGGACAGTAGA
CTGTAGTCAGGAATATGGCAACTAGATTGTACACATTAGAAGGAAGGTATCCTCTGTTAGCAGTTCAATGAGCCAGTG
9 9 c 9 cc 9 9 9 9 9
GATATAGAAGCAGAAGTTTCAAGCAGAAACAGGGCAGGAACACCATATTTTAAATAAACCCATTTTAAATAAACCCATGG
CCAGTAAAACAATACATACGTGCAATGGCAGCAATTCAACGGGTGCTACGGTTAGGGCCCTGTTGCTGGGAAAT
c g c a c t
CAAGCAGGAAATTGG

Figure 13



COMPLETE NUCLEOTIDE SEQUENCE OF p37M-1-10D
AND
AMINO ACID SEQUENCE OF p37^{gag} PROTEIN (SEQ ID NO:129)

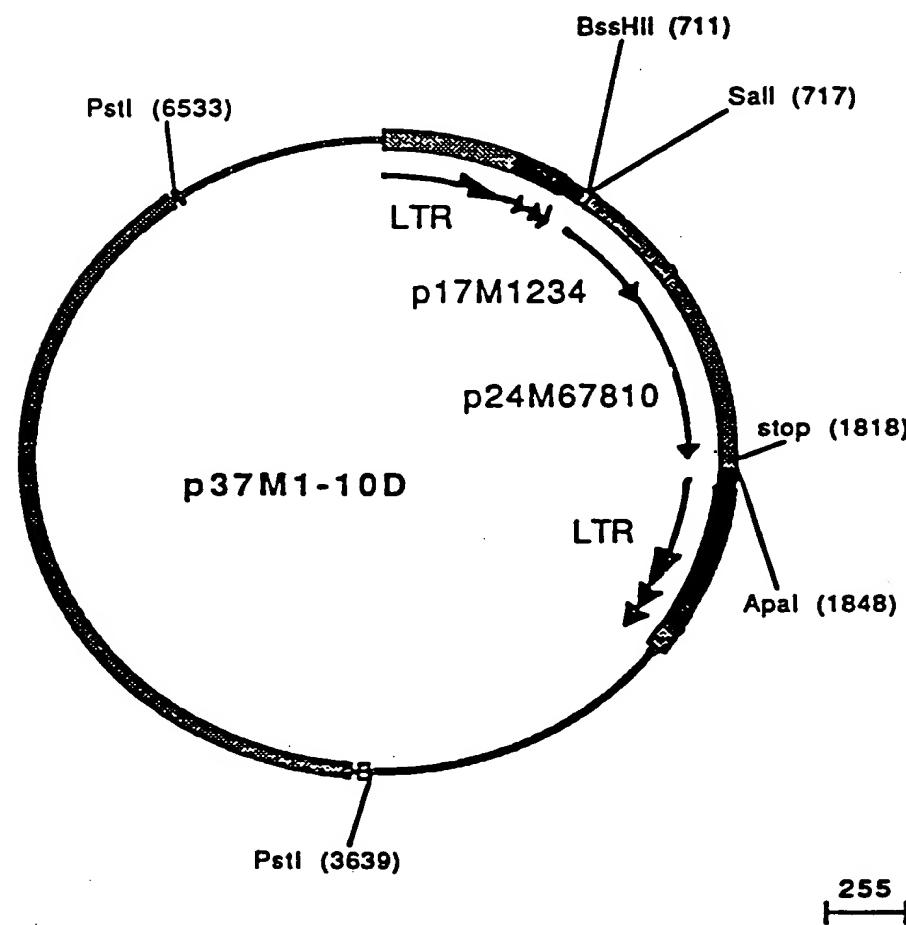


Figure 14



1 TGGAAGGGCT AATTGGTCC CAAAAAGAC AAGAGATCCT TGATCTGTT ATCTACCACA CACAAGGCTA
 71 CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC TGACCTTTGG ATGGTGCTTC
 141 AAGTTAGTAC CAGTGAACC AGAGCAAGTA GAAGAGGCCA AATAAGGAGA GAAGAACAGC TTGTTACACC
 211 CTATGAGCCA GCATGGGAATG GAGGACCCGG AGGGAGAAGT ATTAGTGTGG AAGTTGACA GCCTCCTAGC
 281 ATTCGTCAAC ATGGCCCGAG AGCTGGATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTCTACAGC
 351 GGACTTTCCG CTGGGGACTT TCCAGGGAGG TGTGGCTGG GCGGGACTGG GGAGTGGCGA GCCTCAGAT
 421 GCTACATATA AGCAGCTGCT TTGCTGCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC
 491 TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCT TGAGTGTCTA AAGTAGTGTG
 561 TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC AGACCCCTT AGTCAGTGTG GAAAAATCTCT
 631 AGCAGTGGCG CCCGAACAGG GACTTGAAAG CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG
 BssHII (711)
 701 GCTTGTGAAGCGCGCGTGCACAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGAGAATTAGATCGATGG
 17► Met Glu Arg Ala Ser Val Leu Ser Glu Gly Leu Asp Arg Trp
 777 GAAAAAATTGGTTAAGGCCAGGGGGAAAGAAGAAGTACAAGCTAAAGCACATCGTATGGCAAGCAGGGAGCTAG
 17► Glu Lys Ile Arg Leu Arg Pro Glu Arg Lys Lys Tyr Lys Leu Lys His Ile Val Trp Ala Ser Arg Glu Leu
 853 AACGATTCGAGTTAACCTGGCTGTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAAACATC
 42► Ile Arg Phe Ala Val Asn Pro Glu Leu Leu Glu Thr Ser Glu Gly Cys Arg Glu Ile Leu Glu Leu Glu Pro Ser
 929 CCTTCAGACAGGATCAGAGGAGCTTCGATCACTATACAACACAGTAGCAACCCCTCTATTGTGTGCACCCAGCGGATC
 67► Ile Leu Glu Thr Glu Ser Glu Leu Arg Ser Leu Tyr Asn Thr Val Ala Thr Leu Tyr Cys Val His Glu Ile Arg Ile
 1005 GAGATCAGGACACCAAGGAAGCTTAGACAAGATAGAGGAAGAGCAAAACAGTCCAAGAAGAAGGCCCAGCAGG
 93► Glu Ile Lys Asp Thr Lys Glu Ala Leu Asp Lys Ile Glu Leu Glu Ile Asn Lys Ser Lys Ala Glu Ile Glu Ile
 1081 CAGCAGCTGACACAGGACACAGCAATCAGGTCAAGCCAAAATTACCTATAGTCAGAACATCCAGGGCAAATGGT
 118► Ile Ala Ala Asp Thr Glu His Ser Asn Glu Val Ser Glu Asn Ile Pro Ile Val Glu Ile Lys Ala Phe Ser Pro Glu Val
 1157 ACATCAGGCCATATCACCTAGAACCTTAAATGCATGGTAAAAGTAGTAGAGAGAGAAGGCTTCAGCCCAGAACAGT
 11► Ile His Glu Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Ile Lys Val Val Glu Ile Lys Ala Phe Ser Pro Glu Val
 1233 ATACCCATGTTTCAGCATTATCAGAAGGAGCCACCCACAGGACCTGAACACGATGTTGAACACCGTGGGGGAC
 37► Ile Pro Met Phe Ser Ala Leu Ser Glu Glu Ala Thr Pro Glu Asp Leu Asn Thr Met Leu Asn Thr Val Glu Gly Ile
 1309 ATCAAGCAGCCATGCAAATGTTAAAGAGACCATCAATGAGGAAGCTGCAGAAATGGGATAGAGTCATCCAGTGCA
 62► Ile Glu Ala Ile Met Leu Lys Glu Thr Ile Asn Glu Ala Ile Glu Ile Asn Ile Glu Ile Met Val His Pro Val His
 1385 TGCAGGGCTATTCGACCAAGGCCAGATGAGAGAACCAAGGGAGTGACATAGCAGGAACACTACTAGTACCCCTCAG
 87► Ile Ala Glu Phe Ile Ala Pro Glu Ile Glu Met Arg Glu Pro Arg Glu Ser Asp Ile Ala Glu Ile Thr Thr Ser Thr Leu Glu
 1461 GAACAAATAGGATGGATGACAATAATCCACCTATCCCAGTAGGAGAGATCTACAAGAGGTGGATAATCCGGAT
 113► Glu Ile Glu Ile Glu Trp Met Thr Asn Asn Pro Phe Ile Pro Val Glu Ile Tyr Lys Arg Trp Ile Ile Leu Glu Ile
 1537 TGAACAAGATCGTGAGGAATGTTAGCCCTACCGCAATTCTGGACATAAGACAAGGACCAAGGAACCCCTTAGAGA
 138► Glu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Glu Ile Pro Lys Glu Pro Phe Arg As

Figure 14 continued



1613 CSTATGAGACCGGTTCTATAAACTCTAAGAGCTGAGCAAGCTTCACAGGAGGTAAAAAATTGGATGACAGAACC
 1639 pTyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnGluValLysAsnTrpMetThrGluThr
 1689 TTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCATCCTGAAGGCTCTCGGCCAGCGGCTACACTAGAAGAAA
 1899 LeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGlyProAlaAlaThrLeuGluGlu
 1765 TGATGACAGCATGTCAGGGACTAGGAGGACCCGGCCATAAGGCAAGAGTTTTGTAGGGATCCACTAGTTCTAGACT
 2149 MetThrAlaCysGlnGlyValGlyProGlyHisLysAlaArgValLeu →
 Apal (1848)
 1841 CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTAAA
 1911 AGAAAAGGGG GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC
 1981 CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAAGATAT CCACTGACCT
 2051 TTGGATGGTG CTACAAGCTA GTACCAAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAAG GAGAGAACAC
 2121 CAGCTTGTTA CACCCGTGA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTAGA GTGGAGGTT
 2191 GACAGCCGCC TAGCAATTCA TCACGTGGCC CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC
 2261 GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTTCCAGG GAGGGCTGGC CTGGGGGGGA CTGGGGAGTG
 2331 GCGAGCCCTC AGATGCTGCA TATAAGCAGC TGCTTTTGC CTGTAAGGGGG TCTCTCTGGT TAGACCAGAT
 2401 CTGAGCCTGG GAGCTCTCTG GCTAACTAGG GAACCCACTG CTTAAGCTC AATAAAGCTT GCCTTGAGTG
 2471 CTTCAAGTAG TGTGTGCCCG TCTGTTGTT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG
 2541 TGTGGAAAAT CTCTAGCACC CCCCAGGAGG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA CTGCATTCCA
 2611 GCCTGGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG TATTTAAATAT ATTATATACAT
 2681 GGAGGTCTATA AAAATATATA TATTTGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTGGGAGG
 2751 CCGAGGCAGG TGGATCACCT GAGTTTGGGA GTTCCAGACCC AGCCTGACCA ACATGGAGAA ACCCCCTCTC
 2821 TGTGTATTT TAGTAGATTT TATTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAAACTGTT
 2891 TTCCCTCTAC TCTGATAACCA CAAGAATCAT CAGCACAGAG GAAGACTCT GTGATCAAAT GTGGTGGGAG
 2961 AGGGAGGTTT TCACCAAGCAC ATGAGCAGTC AGTTCTGCCG CAGACTCGGC GGGTGTCCCT CGGTTCAAGTT
 3031 CCAACACCCG CTGCGCTGGAG AGAGGTCTAGA CCACAGGGTG AGGGCTCAGT CCCCAGACAA TAAACACCC
 3101 AGACATAAAC ACCAACACAGG TCCACCCCGC CTGCTGCCCCA GGCAAGGGCC ATTACCAAG ACGGGAAITA
 3171 GGATAGAGAA AGAGTAAGTC ACACAGAGCC GGCCTGTGCGG GAGAACGGAG TTCTATTAAG ACTCAAATCA
 3241 GTCTCCCCAA GCATTGGGG ATCAGAGTTT TTAAGGATAA CTTAGTTGTT AGGGGGCCAG TGAGTTGGAG
 3311 ATGAAAGCGT AGGGAGTCGA AGGTGTCTT TTGCGCCGAG TCAGTTCTG GGTGGGGGCC ACAAGATCGG
 3381 ATGAGCCAGT TTATCAATCC GGGGGTGCCTA GCTGATCCAT GGAGTGCAGG GTCTGCAAA TATCTCAAGC
 3451 ACTGATTGAT CTTAGTTTT ACAATAGTA TGTTACCCCA GGAACAAATT GGGGAAGGTC AGAATCTGT
 3521 AGCTGTAGC TGCATGACTC CTAACACATA ATTCTTTTT TGTTTTTTT TTTTATTT TGAGACAGGG
 PsiII (3639)
 3591 TCTCACTCTG TCACCTAGGC TGGAGTGCAG TGGTGCATC ACAGCTCACT GCAGCCCTA GAGCGGCCGC
 3661 CACCGCGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGA TTACAATCA CTGGCCGTGCG TTTTACAACG
 3731 TCGTGAATGG GAAAACCTG GCGTTACCCCA ACTTAATCGC CTGCAAGCAC ATCCCCCTTT CGCCAGCTGG
 3801 CGTAATAGCG AAGAGGCCCG CACCGATCGC CTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGCGCG
 3871 AAATTGTTAA CGTTAAATT TTGTTAAAAT TCGCGTTAAA TTTTGTAA ATCAGCTCAT TTTTTAACCA
 3941 ATAGGCGCAA ATCGGCAAA TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTTCCA
 4011 GTTTGGAAACA AGAGTCACCT ATTAAGAAC GTGGACTCCA ACGTCAAAGG GCGAAAAAAC GTCATATCAGG
 4081 CGGATGGGCCCG ACTACGTGAA CCATCACCCCT ATCAAGTTT TTGGGGTCG AGGTGCGCTA AAGCACTAA
 4151 TCGGAACCCCT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG CGAACGTTGGC GAGAAAGGAA
 4221 GGGAAAGAAAG CGAAAGGAGC GGGCGCTAGG CGCTGGCAA GTGTAGGGT CACCGTGCAGC GTAAACACCA
 4291 CACCCGCCGC GCTTAATGG CCGCTACAGG GCGCTGCCCA GTGGCACTT TTGGGGAAA TGTCGGCGGA
 4361 ACCCCCTATTT TTGTTATTT CTAATACAT TCAAAATATGT ATCCGCTCAT GAGACAATAA CCGCTGATAAA

Figure 14 continued



4431 TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTGCCCTTA TTCCCTTTT
 4501 TGCAGGCAATT TGCCCTTCTG TTTTGCTCA CCCAGAAACG CTGGTGAAG TAAAGATGC TGAAGATCAG
 4571 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCG
 4641 AAGAACGTTT TCCAATGATG AGCACTTTA AAGTTCGCT ATGTGGCGC GTATTATCCC GTATTGACCC
 4711 CGGGCAAGAG CAACTCGGTC GCGGCATACA CTATTCTAG AATGACTTGG TTGAGTACTC ACCAGTCACA
 4781 GAAAAGCATT TTACGGATGG CATGACAGTA AGAGAAATTAT GCAGTGCCTGC CATAACCATG AGTGATAACA
 4851 CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAAC GCTTTTTGC ACAACATGGG
 4921 GGATCAATGTA ACTCGCCCTG ATCGTTGGGA ACCGGAGCTG AATGAACCA TACCAACGA CGAGCGTGA
 4991 ACCACGATGC CTGTTAGCAACG TGCGCCTAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT
 5061 CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGAGGAGCCA CCTTCGCGCT CGGGCCCTTC
 5131 GGCTGGCTGG TTATTCGTTG ATAAATCTGG AGCCGGTGTAG CGTGGGTCTC GCGGTATCAT TGAGCACTG
 5201 GGGCCAGATG GTAAGCCCTC CCGTATCGTA TTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
 5271 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTTGGTAA CTGTCAGACC AAGTTTACTC
 5341 ATATATACCTT TAGATTGATT TAAAACCTCA TTTTTAATTAA AAAAGGATCT AGGTGAAGAT CCTTTTTGAT
 5411 AATCTCATGA CCAAAATCCC TTAACTGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA
 5481 AAGGATCTTC TTGAGATCTC TTTTCTGC GCGTAATCTG CTGCTTGCCTA ACAAAAAAAC CACCGCTACC
 5551 AGCGGTGGTT TGTGCGGGG ATCAAGAGCT ACCAATCTT TTCCGAGGG TAATGGCTT CAGCAGAGCG
 5621 CAGATACCAA ATACTGTCTC TCTAGTGTAG CGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC
 5691 CTACATACCT CGCTCTGCTA ATCTGTCTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTAACCGG
 5761 GTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTG GTGCACACAG
 5831 CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGOTGTA GCTATGAGAA AGCGCCACGC
 5901 TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGG
 5971 GCTTCCAGGG GGAAACGCTT GGTATCTTTA TAGTCTGTC GGGTTTGGC ACCTCTGACT TGAGGCTCGA
 6041 TTTTGTGAT GCTCGTCAGG GGGCGGGAGC CTATGGAAAA ACGCCAGCAA CGCGCCCTT TTACGGTCTC
 6111 TGGCCTTTTG CTGGCTTTTGT GCTCACATGT TCTTTCTGC TTATCCCT GATTCTGTGG ATAACCGTAT
 6181 TACCGCTTTG GAGTGGCTG ATACCGCTCG CGCAGCCGA ACAGCCGAGC GCAGCGAGTC AGTGGAGCG
 6251 GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTGGCC GATTCACTAA TGAGCTGGC
 6321 ACGACAGGTT TCCCAGCTGG AAAGCGGGCA GTGAGGCAA CGCAATTAA TGAGATAGC TCACTCACTA
 6391 GGCACCCCCAG GCTTACACT TTATGCTTCC GGCTGTATG TTGTGTGGAA TTGTGAGCGG ATAACCAATT
 6461 CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC
 PsiI (6533)
 6531 TGCTGCAGGG TCCCTAACTG CCAAGCCCCA CAGTGTGCC TGAGGCTGCC CCTTCCTCT AGCGGCTGCC
 6601 CCCACTCGGC TTGCTTCTC CTAGTTTCAG TTACTTGCCT TCAGCCAAGG TCTGAAACTA GTGCGCACA
 6671 GAGCGGTAAAG ACTGCGAGAG AAAGGACCA GCTTACAGG GGGTTTATCA CAGTGCACCC TGACAGTCGT
 6741 CAGCCTCACA GGGGGTTTAT CACATTGAC CCTGACAGTC GTCAAGCTC CAGGGGGTTT ATCACAGTC
 6811 ACCCTTACAA TCATTCCATT TGATTACAA TTTTTTGT CTCTACTGTG CCTAACTTGT AAGTTAAATT
 6881 TGATCAGAGG TGTTTCTCA GAGGGGGAAA CAGTATATAC AGGGTTCACT ACTATCGCAT TTCAAGGCCCTC
 6951 CACCTGGGTC TTGGAATGTG TCCCCCGAGG GTGTATGACT ACCTCAGTGT GATCTCCACA GGTACAGTG
 7021 ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCAACATG GGCGCCCTC CACGTGCACA TGGCCGGAGG
 7091 AACTGCCATG TCGGAGGTGC AAGCACACCT GGGCATCAGA GTCCCTGGTG TGGAGGGAGG GACCAGCGCA
 7161 GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG CCCCAGTTCT ACTTACACCA GGAAAGGC

Figure 14 continued